polypeptide fragment of at least about 25 amino acid residues wherein the polypeptide fragment has an activity of the encoded polypeptide as set forth in SEQ ID NO: 5, or is antigenic.

3. (Amended) An isolated nucleic acid molecule comprising:

(a) a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 5 with at least one modification that is a conservative amino acid substitution, C-terminal truncation, or N-terminal truncation, wherein the encoded polypeptide has an activity of the polypeptide as set forth in SEQ ID NO: 5; or

(b) a nucleotide sequence complementary to the nucleotide sequence of (a).

Please cancel claims 10, 11, and 46-48 without prejudice or disclaimer.

REMARKS

The Examiner indicated that claims 1-8, 10, 11, and 46-48 were pending at the issuance of the instant Office Action. Claims 1-3 have been amended and claims 10, 11, and 46-48 have been canceled. The amendments to the claims are fully supported by the specification. No new matter has been added as a result of the above-described amendments. The rejections set forth in the Office Action have been overcome by amendment or are traversed by argument below.

1. Objection to claims 1-8, 10, 11, and 46-48

The Office Action contains an objection to claims 1-8, 10, 11, and 46-48 as being drawn in the alternative to a non-elected invention. Applicants have amended claims 1-3 to recite only the elected invention.

2. Rejections of claims 1-8, 10, 11, and 46-48 under 35 U.S.C. § 112, first paragraph

The Office Action contains a rejection of claims 1-8, 10, 11, and 46-48 under 35 U.S.C. § 112, first paragraph, as not being enabling for an isolated nucleic acid molecule comprising a nucleotide sequence that hybridizes under moderately or highly stringent conditions to the complement of the nucleotide sequence set forth in SEQ ID NO: 4 or an isolated nucleic acid molecule encoding an isolated polypeptide comprising an amino acid sequence that is at least about

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70% identical to the amino acid sequence set forth in SEQ ID NO: 5. The Examiner takes the position that, given the broadest reasonable interpretation, the breadth of the claims in the present application encompasses any and all isolated nucleic acid molecules that encode a polypeptide.

Applicants respectfully contend that since the claims of the present application are drawn to an isolated nucleic acid molecule encoding an isolated polypeptide comprising an amino acid sequence that is *at least about 70% identical* to the amino acid sequence set forth in SEQ ID NO: 5, wherein the encoded polypeptide *possesses an activity of the polypeptide* set forth in SEQ ID NO: 5, the breadth of the claims cannot encompass any and all isolated nucleic acid molecules. Most nucleic acid molecules will encode polypeptides that share *less than* 70% amino acid sequence identity to the polypeptide set forth in SEQ ID NO: 5, or *lack* an activity of the polypeptide set forth in SEQ ID NO: 5. Nevertheless, in an effort to expedite prosecution of the pending claims to allowance, Applicants have amended the claims to recite nucleic acid molecules encoding polypeptides having the amino acid sequence as set forth in SEQ ID NO. 5, or having conservative substitutions or N- or C-terminal truncations of said sequence. Applicants, having deleted the objected-to limitation of "at least about 70% identical" from the pending claims, respectfully contend that this ground of rejection has been overcome. Applicants further contend that by deleting claim 1(d) – which is directed in part to an isolated nucleic acid molecule comprising a nucleotide sequence that hybridizes under moderately or highly stringent conditions to the complement of the nucleotide sequence set forth in SEQ ID NO: 4 – this ground of the rejection has also been overcome. Withdrawal of this rejection is therefore respectfully solicited.

The Examiner also takes the position that since the introduction of a particular amino acid substitution in a polypeptide variant may affect the structure or function of that polypeptide variant, one with skill in the art cannot make and use the claimed invention without undue experimentation. However, as the Examiner notes, Bowie *et al.* teach that even regions critical to the three-dimensional structure/function relationship can tolerate conservative substitutions. Applicants have amended the pending claims to recite nucleic acid molecules encoding sequence variants of explicitly disclosed SEQ ID NO. 5 comprising conservative substitutions. As supported by the Bowie *et al.* reference cited by the Examiner, provision of particular species of nucleic acid molecules encoding polypeptides possessing these types of substitutions do not entail undue

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experimentation, since one of ordinary skill in the art would expect that the purportedly critical structure/activity relationships would be retained in the encoded polypeptide variants. Applicants respectfully submit that the claims as amended fulfill the requirements of 35 U.S.C. § 112, first paragraph, and request that the Examiner withdraw this ground of rejection.

3. Rejections of claims 46-48 under 35 U.S.C. § 112, first paragraph

The Office Action contains a rejection of claims 46-48 under 35 U.S.C. § 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention. The Examiner takes the position that the specification cannot be extrapolated to enable claims drawn to a pharmaceutical composition comprising a nucleic acid molecule or fragment thereof encoding a polypeptide or a fragment thereof comprising an amino acid sequence that is at least about 70% identical to the amino acid sequence set forth in SEQ ID NO: 5. In order to expedite prosecution of the instant application, Applicants have canceled claims 46-48 without prejudice or disclaimer, rendering this rejection moot. This amendment has been made solely to expedite prosecution and was not made to overcome prior art.

4. Rejections of claims 1-8, 10, 11, and 46-48 under 35 U.S.C. § 112, first paragraph

The Office Action contains a rejection of claims 1-8, 10, 11, and 46-48 under 35 U.S.C. § 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the claimed invention. The Examiner takes the position that the disclosure of the nucleic acid sequences set forth in SEQ ID NO: 1, SEQ ID NO: 4, and SEQ ID NO: 8 does not reasonably convey to one skilled in the relevant art that the inventors had possession of the genus of nucleic acid molecules which encode Secs-1 polypeptides having at least 70% identity to the amino acid sequence set forth in SEQ ID NO: 5, or of nucleic acid molecules encoding Secs-1 allelic or splice variants. As discussed in paragraph 3 above, the objected-to limitation of "at least about 70% identical" has been deleted from the pending claims, and therefore, Applicants respectfully contend that this ground of rejection has been overcome.

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The Examiner also takes the position that lack of disclosure as to the structure and sequence of the native promoter for the human Secs-1 gene suggests that the Applicants did not have possession of nucleic acid molecules comprising promoter DNA other than the promoter DNA for the native Secs-1 polypeptide. Applicants, having canceled claim 10, contend that this ground of rejection has been rendered moot. Withdrawal of this rejection is therefore respectfully solicited.

5. Rejections of claims 1-8, 10, 11, and 46-48 under 35 U.S.C. § 112, second paragraph

The Office Action contains a rejection of claims 1-8, 10, 11, and 46-48 under 35 U.S.C. § 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which Applicants regard as the invention. The Examiner takes the position that claims 1-8, 10, 11, and 46-48 are vague and indefinite because claims 2 and 3 recite the phrase "has an activity." Applicants contend, however, that claims containing this limitation encompass only those nucleic acid molecules encoding Secs-1 polypeptide variants that possess an inherent activity of the polypeptide as set forth in SEQ ID NO: 5. Applicants teach the expression of human Secs-1 mRNA in colon and prostate tissue (page 97, lines 13-14), and strong expression of murine Secs-1 mRNA in the epithelial cells of the gastrointestinal system (page 88, line 26 to page 89, line 2). The expression of Secs-1 polypeptides in these tissues indicates that Secs-1 polypeptide has an inherent function. In view of the inherency of activity that resides in polypeptides having the amino acid sequence as set forth in SEQ ID NO. 5, Applicants respectfully contend that the term is not indefinite and that the claims fulfills the requirements of 35 U.S.C. § 112, second paragraph.

The Examiner also takes the position that claims 1-8, 10, 11, and 46-48 are indefinite because claims 1-3 recite the phrase "the DNA insert in ATCC Deposit Nos. PTA-1753 and PTA-1755." Applicants have amended claims 1-3 to recite only the elected invention, thus overcoming this rejection.

The Examiner also takes the position that claims 1-8, 10, 11, and 46-48 are indefinite because claim 1 recites the phrase "hybridizes under moderately or highly stringent conditions." While Applicants note that the specification defines the meaning of the terms "moderately stringent conditions" (page 18, lines 8-14) and "highly stringent conditions" (page 17, lines 3-10), and provides examples of each, Applicants have amended the pending claims without prejudice or

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disclaimer in an effort to expedite the present application to allowance.

The Examiner also takes the position that claim 11 is indefinite for failing to identify the algorithm and software by the version and the date of the version. Applicants have canceled claim 11 without prejudice or disclaimer, rendering this rejection moot.

Applicants respectfully contend that rejections based on 35 U.S.C. § 112, second paragraph, have been overcome by amendment, traversed by argument, or mooted by cancellation of the rejected claims, and request that the Examiner withdraw all rejections made on this basis.

6. Rejections of claims 2, 3, and 11 under 35 U.S.C. § 102

The Office Action contains a rejection of claims 2, 3, and 11 under 35 U.S.C. § 102(a), as being anticipated by the FAPESP/LICR Human Cancer Genome Project (GenBank EST Database Accession No. AW351839), contending that the FAPESP/LICR Human Cancer Genome Project teach the nucleotide sequence of an isolated nucleic acid molecule encoding an amino acid sequence that is 100% identical to the amino acid sequence set forth in SEQ ID NO: 5. The Office Action also contains a rejection of claims 2, 3, and 11 under 35 U.S.C. § 102(b), as being anticipated by Hillier *et al.* (GenBank EST database Accession No. AA422178), contending that Hillier *et al.* teach the nucleotide sequence of an isolated nucleic acid molecule encoding an amino acid sequence that is 100% identical to the amino acid sequence set forth in SEQ ID NO: 5 over the region spanning from the amino acid at position 1 to the amino acid at position 76. Applicants traverse these rejections.

Applicants first note that while GenBank Accession Nos. AA422178 (published October 16, 1997) and AW351839 (published February 1, 2000) disclose EST sequences of 503 bp and 356 bp, respectively, neither reference teaches the amino acid sequence of Secs-1 polypeptide. With regard to the nucleotide sequence disclosed in GenBank Accession No. AW351839, Applicants submit a Declaration under 37 C.F.R. § 1.131 establishing invention of the subject matter of the claims rejected under 35 U.S.C. § 102(a) prior to the effective date of the reference on which the rejection is based.

Applicants also submit herewith a nucleotide sequence alignment (Appendix A) showing that the nucleotide sequence as disclosed in GenBank Accession No. AA422178 (Hillier *et al.*) is not identical to the nucleotide sequence as set forth in SEQ ID NO: 4. Applicants contend that because

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the nucleotide sequence disclosed by Hillier *et al.* lacks the nucleotide found at position 258 in the nucleotide sequence of SEQ ID NO: 4, the nucleotide sequence disclosed by Hillier *et al.* does not encode the polypeptide set forth in SEQ ID NO: 5. Moreover, Hillier *et al.* does not teach the amino acid sequence of *any* protein, and one of ordinary skill in the art would be unable to determine – *absent the teaching of the instant application* – which among the multiple open reading frames in the nucleotide sequence of Hillier *et al.* encode a translated protein. In addition, Applicants note that using the teaching of the instant application, one of ordinary skill in the art would determine that the polypeptide encoded by the nucleotide sequence of Hillier *et al.* differs from the polypeptide set forth in SEQ ID NO: 5 at positions 77-81 and possesses an additional 17 amino acids at its C-terminal end. Furthermore, Applicants contend that the substitution of the stop codon at positions 272-274 in the nucleotide sequence of SEQ ID NO: 4 with a codon for serine in the nucleotide sequence of Hillier *et al.* does not constitute a conservative substitution, and therefore, Hillier *et al.* does not anticipate isolated nucleic acid molecules comprising a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 5 with at least one modification that is a conservative amino acid substitution, wherein the encoded polypeptide has an activity of the polypeptide as set forth in SEQ ID NO: 5. Applicants therefore respectfully request the Examiner to withdraw the rejections of claims 2 and 3 on 35 U.S.C. § 102 grounds.

7. Rejections of claims 1-8, 10, and 11 under 35 U.S.C. § 103(a)

The Office Action contains a rejection of claims 1-8, 10, and 11 under 35 U.S.C. § 103(a), as being unpatentable over the FAPESP/LICR Human Cancer Genome Project (GenBank EST Database Accession No. AW351839). The Examiner takes the position that it would have been *prima facie* obvious to one of ordinary skill in the art, at the time the invention was made, to make and use an expression vector comprising the nucleic acid molecule of the FAPESP/LICR Human Cancer Genome Project to produce a polypeptide comprising the amino acid sequence of SEQ ID NO: 5. The Office Action also contains a rejection of claims 1-8, 10, and 11 under 35 U.S.C. § 103(a), as being unpatentable over Hillier *et al.* (GenBank EST database Accession No. AA422178). The Examiner takes the position that it would have been *prima facie* obvious to one of ordinary skill in the art, at the time the invention was made, to make and use an expression vector comprising the

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nucleic acid molecule of Hillier *et al.* to produce a polypeptide comprising the amino acid sequence of SEQ ID NO: 5. Applicants traverse these rejections.

As discussed in paragraph 6 above, Applicants submit a Declaration under 37 C.F.R. § 1.131 establishing invention of the subject matter of claims 1-8, 10, and 11 prior to the effective date of the FAPESP/LICR Human Cancer Genome Project. Therefore, Applicants contend that the claims are not obvious under 35 U.S.C. § 103 with respect to this reference, and request the Examiner withdraw this rejection. As also discussed in paragraph 6, the nucleotide sequence disclosed by Hillier *et al* differs from that set forth in SEQ ID NO: 4 (resulting in a frame shift that would produce a polypeptide differing at positions 77-81 and possessing an additional 17 amino acids at its C-terminal end). Therefore, Applicants contend that one of ordinary skill in the art would be unable to make and use an expression vector comprising a nucleic acid molecule encoding a polypeptide comprising the amino acid sequence of SEQ ID NO: 5. Furthermore, Applicants contend that the substitution of the stop codon at positions 272-274 in the nucleotide sequence of SEQ ID NO: 4 with a codon for serine in the nucleotide sequence of Hillier *et al.* does not constitute a conservative substitution, and therefore, one of ordinary skill in the art would be unable to make and use an expression vector comprising a nucleic acid molecule encoding a polypeptide comprising the amino acid sequence of SEQ ID NO: 5 with at least one modification that is a conservative amino acid substitution, wherein the encoded polypeptide has an activity of the polypeptide as set forth in SEQ ID NO: 5. Applicants therefore respectfully contend that the claims are not obvious under 35 U.S.C. § 103 with respect to Hillier *et al.*, and request the Examiner withdraw this rejection.

CONCLUSIONS

Applicants respectfully contend that all conditions of patentability are met in the pending claims as amended. Allowance of the claims is thereby respectfully solicited. If Examiner Rawlings believes it to be helpful, he is invited to contact the undersigned representative by telephone at (312) 913-0001.

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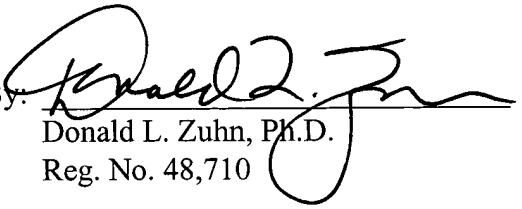
Respectfully submitted,
McDonnell Boehnen Hulbert & Berghoff

Dated: February 11, 2002

By: 
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AMENDMENTS TO THE CLAIMS

Marked Up Versions of Amended Claims under 37 C.F.R. 1.121(c)(1)(ii)

1. (Amended) An isolated nucleic acid molecule comprising ~~a nucleotide sequence selected from the group consisting of~~:

(a) the nucleotide sequence as set forth in ~~SEQ ID NO: 1 or~~ SEQ ID NO: 4;

(b) the nucleotide sequence of the DNA insert in ATCC Deposit Nos. ~~PTA-1753 or~~ PTA-1755;

(c) a nucleotide sequence encoding the polypeptide as set forth in ~~SEQ ID NO: 2 or~~ SEQ ID NO: 5; or

~~(d) a nucleotide sequence which hybridizes under moderately or highly stringent conditions to the complement of any of (a) - (c); and~~

~~(e)~~(d) a nucleotide sequence complementary to any of (a) - (c).

2. (Amended) An isolated nucleic acid molecule comprising ~~a nucleotide sequence selected from the group consisting of:~~

~~(a) a nucleotide sequence encoding a polypeptide that is at least about 70 percent identical to the polypeptide as set forth in SEQ ID NO: 2 or SEQ ID NO: 5 wherein the encoded polypeptide has an activity of the polypeptide set forth in SEQ ID NO: 2 or SEQ ID NO: 5;~~

~~(b) a nucleotide sequence encoding an allelic variant or splice variant of the nucleotide sequence as set forth in SEQ ID NO: 1 or SEQ ID NO: 4, the nucleotide sequence of the DNA insert in ATCC Deposit Nos. PTA-1753 or PTA-1755, or (a);~~

~~(c)~~ a region of the nucleotide sequence of ~~SEQ ID NO: 1,~~ SEQ ID NO: 4~~,~~ or the DNA insert in ATCC Deposit Nos. ~~PTA-1753 or~~ PTA-1755~~, (a), or (b)~~ encoding a polypeptide fragment of at least about 25 amino acid residues wherein the polypeptide fragment has an activity of the encoded polypeptide as set forth in ~~SEQ ID NO: 2 or~~ SEQ ID NO: 5, or is antigenic~~;~~

~~(d) a region of the nucleotide sequence of SEQ ID NO: 1, SEQ ID NO: 4, the DNA insert in ATCC Deposit Nos. PTA-1753 or PTA-1755, or any of (a) - (c) comprising a fragment of at least about 16 nucleotides;~~

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~~(e) a nucleotide sequence which hybridizes under moderately or highly stringent conditions to the complement of any of (a) - (d); and~~

~~(f) a nucleotide sequence complementary to any of (a) - (d).~~

3. (Amended) An isolated nucleic acid molecule comprising ~~a nucleotide sequence selected from the group consisting of~~:

~~(a) a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 or SEQ ID NO: 5 with at least one conservative amino acid substitution, wherein the encoded polypeptide has an activity of the polypeptide as set forth in SEQ ID NO: 2 or SEQ ID NO: 5;~~

~~(b) a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 or SEQ ID NO: 5 with at least one amino acid insertion, wherein the encoded polypeptide has an activity of the polypeptide as set forth in SEQ ID NO: 2 or SEQ ID NO: 5;~~

~~(c) a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 or SEQ ID NO: 5 with at least one amino acid deletion, wherein the encoded polypeptide has an activity of the polypeptide as set forth in SEQ ID NO: 2 or SEQ ID NO: 5;~~

~~(d) a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 or SEQ ID NO: 5 which has a C- and/or N- terminal truncation, wherein the encoded polypeptide has an activity of the polypeptide as set forth in SEQ ID NO: 2 or SEQ ID NO: 5;~~

~~(e)~~(a) a nucleotide sequence encoding a polypeptide as set forth in ~~SEQ ID NO: 2 or~~ SEQ ID NO: 5 with at least one modification ~~selected from the group consisting of~~ that is a conservative amino acid substitutions, ~~amino acid insertions, amino acid deletions,~~ C-terminal truncation, ~~and~~or N-terminal truncation, wherein the encoded polypeptide has an activity of the polypeptide as set forth in ~~SEQ ID NO: 2 or~~ SEQ ID NO: 5; or

~~(f) a nucleotide sequence of any of (a) - (e) comprising a fragment of at least about 16 nucleotides;~~

~~(g) a nucleotide sequence which hybridizes under moderately or highly stringent conditions to the complement of any of (a) - (f); and~~

~~(h)~~(b) a nucleotide sequence complementary to ~~any of~~the nucleotide sequence of (a) ~~- (e)~~.

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